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SEQUENCE LISTING

<110> Jackson, Stephen P  
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<120> Assays, agents, therapy and diagnosis relating to  
modulation of cellular DNA repair activity

<130> MEWE-005

<140> US 09/341,505

<141> 1999-07-12

<150> PCT/GB98/00095

<151> 1998-01-13

<150> GB 9700574.8

<151> 1997-01-13

<150> GB 9713131.2

<151> 1997-06-20

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<170> PatentIn Ver. 2.1

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                   20                  25                  30  
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			20					25					30				
Pro	Asp	Phe	Lys	Trp	Leu	Cys	Glu	Glu	Leu	Phe	Val	Lys	Ile	His	Glu		
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Val	Gln	Ile	Asn	Gly	Thr	Ala	Gly	Thr	Gly	Lys	Ser	Arg	Ser	Phe	Lys		
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Tyr	Tyr	Glu	Ile	Ile	Ser	Asn	Phe	Val	Glu	Met	Trp	Arg	Lys	Thr	Val		
65					70					75					80		
Gly	Asn	Asn	Ile	Tyr	Pro	Ala	Leu	Val	Leu	Ala	Leu	Pro	Tyr	Arg	Asp		
				85					90						95		
Arg	Arg	Ile	Tyr	Asn	Ile	Lys	Asp	Tyr	Val	Leu	Ile	Arg	Thr	Ile	Cys		
			100					105						110			
Ser	Tyr	Leu	Lys	Leu	Pro	Lys	Asn	Ser	Ala	Thr	Glu	Gln	Arg	Leu	Lys		
		115					120					125					
Asp	Trp	Lys	Gln	Arg	Val	Gly	Lys	Gly	Gly	Asn	Leu	Ser	Ser	Leu	Leu		
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Val	Glu	Glu	Ile	Ala	Lys	Arg	Arg	Ala	Glu	Pro	Ser	Ser	Lys	Ala	Ile		
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Thr	Ile	Asp	Asn	Val	Asn	His	Tyr	Leu	Asp	Ser	Leu	Ser	Gly	Asp	Arg		
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Phe	Ala	Ser	Gly	Arg	Gly	Phe	Lys	Ser	Leu	Val	Lys	Ser	Lys	Pro	Phe		
			180					185					190				
Leu	His	Cys	Val	Glu	Asn	Met	Ser	Phe	Val	Glu	Leu	Lys	Tyr	Phe	Phe		
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				245					250					255			
Lys	Asp	Asp	Asp	Leu	Ser	Ile	Lys	Val	Gly	Phe	Ala	Phe	Ala	Pro	Gln		
			260					265					270				
Leu	Ala	Lys	Lys	Val	Asn	Leu	Ser	Tyr	Glu	Lys	Ile	Cys	Arg	Thr	Leu		
		275					280					285					
His	Asp	Asp	Phe	Leu	Val	Glu	Glu	Lys	Met	Asp	Gly	Glu	Arg	Ile	Gln		
	290					295					300						
Val	His	Tyr	Met	Asn	Tyr	Gly	Glu	Ser	Ile	Lys	Phe	Phe	Ser	Arg	Arg		
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Gly Ile Asp Tyr Thr Tyr Leu Tyr Gly Ala Ser Leu Ser Ser Gly Thr  
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 340 345 350  
 Asp Gly Glu Met Val Thr Phe Asp Ala Lys Arg Arg Val Ile Leu Pro  
 355 360 365  
 Phe Gly Leu Val Lys Gly Ser Ala Lys Glu Ala Leu Ser Phe Asn Ser  
 370 375 380  
 Ile Asn Asn Val Asp Phe His Pro Leu Tyr Met Val Phe Asp Leu Leu  
 385 390 395 400  
 Tyr Leu Asn Gly Thr Ser Leu Thr Pro Leu Pro Leu His Gln Arg Lys  
 405 410 415  
 Gln Tyr Leu Asn Ser Ile Leu Ser Pro Leu Lys Asn Ile Val Glu Ile  
 420 425 430  
 Val Arg Ser Ser Arg Cys Tyr Gly Val Glu Ser Ile Lys Lys Ser Leu  
 435 440 445  
 Glu Val Ala Ile Ser Leu Gly Ser Glu Gly Val Val Leu Lys Tyr Tyr  
 450 455 460  
 Asn Ser Ser Tyr Asn Val Ala Ser Arg Asn Asn Asn Trp Ile Lys Val  
 465 470 475 480  
 Lys Pro Glu Tyr Leu Glu Glu Phe Gly Glu Asn Leu Asp Leu Ile Val  
 485 490 495  
 Ile Gly Arg Asp Ser Gly Lys Lys Asp Ser Phe Met Leu Gly Leu Leu  
 500 505 510  
 Val Leu Asp Glu Glu Glu Tyr Lys Lys His Gln Gly Asp Ser Ser Glu  
 515 520 525  
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 530 535 540  
 Arg Val Lys Lys Ile Leu Ser Phe Cys Ser Ile Ala Asn Gly Ile Ser  
 545 550 555 560  
 Gln Glu Glu Phe Lys Glu Ile Asp Arg Lys Thr Arg Gly His Trp Lys  
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 Arg Thr Ser Glu Val Ala Pro Pro Ala Ser Ile Leu Glu Phe Gly Ser  
 580 585 590  
 Lys Ile Pro Ala Glu Trp Ile Asp Pro Ser Glu Ser Ile Val Leu Glu  
 595 600 605  
 Ile Lys Ser Arg Ser Leu Asp Asn Thr Glu Thr Asn Met Gln Lys Tyr  
 610 615 620

Ala	Thr	Asn	Cys	Thr	Leu	Tyr	Gly	Gly	Tyr	Cys	Lys	Arg	Ile	Arg	Tyr	625	630	635	640
Asp	Lys	Glu	Trp	Thr	Asp	Cys	Tyr	Thr	Leu	Asn	Asp	Leu	Tyr	Glu	Ser	645	650	655	
Arg	Thr	Val	Lys	Ser	Asn	Pro	Ser	Tyr	Gln	Ala	Glu	Arg	Ser	Gln	Leu	660	665	670	
Gly	Leu	Ile	Arg	Lys	Lys	Arg	Lys	Arg	Val	Leu	Ile	Ser	Asp	Ser	Phe	675	680	685	
His	Gln	Asn	Arg	Lys	Gln	Leu	Pro	Ile	Ser	Asn	Ile	Phe	Ala	Gly	Leu	690	695	700	
Leu	Phe	Tyr	Val	Leu	Ser	Asp	Tyr	Val	Thr	Glu	Asp	Thr	Gly	Ile	Arg	705	710	715	720
Ile	Thr	Arg	Ala	Glu	Leu	Glu	Lys	Thr	Ile	Val	Glu	His	Gly	Gly	Lys	725	730	735	
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Gly	Tyr	Asp	Ile	Leu	His	Pro	Asn	Trp	Val	Leu	Asp	Cys	Ile	Ala	Tyr	770	775	780	
Lys	Arg	Leu	Ile	Leu	Ile	Glu	Pro	Asn	Tyr	Cys	Phe	Asn	Val	Ser	Gln	785	790	795	800
Lys	Met	Arg	Ala	Val	Ala	Glu	Lys	Arg	Val	Asp	Cys	Leu	Gly	Asp	Ser	805	810	815	
Phe	Glu	Asn	Asp	Ile	Ser	Glu	Thr	Lys	Leu	Ser	Ser	Leu	Tyr	Lys	Ser	820	825	830	
Gln	Leu	Ser	Leu	Pro	Pro	Met	Gly	Glu	Leu	Glu	Ile	Asp	Ser	Glu	Val	835	840	845	
Arg	Arg	Phe	Pro	Leu	Phe	Leu	Phe	Ser	Asn	Arg	Ile	Ala	Tyr	Val	Pro	850	855	860	
Arg	Arg	Lys	Ile	Ser	Thr	Glu	Asp	Asp	Ile	Ile	Glu	Met	Lys	Ile	Lys	865	870	875	880
Leu	Phe	Gly	Gly	Lys	Ile	Thr	Asp	Gln	Gln	Ser	Leu	Cys	Asn	Leu	Ile	885	890	895	
Ile	Ile	Pro	Tyr	Thr	Asp	Pro	Ile	Leu	Arg	Lys	Asp	Cys	Met	Asn	Glu	900	905	910	
Val	His	Glu	Lys	Ile	Lys	Glu	Gln	Ile	Lys	Ala	Ser	Asp	Thr	Ile	Pro	915	920	925	

15

Lys Ile Ala Arg Val Val Ala Pro Glu Trp Val Asp His Ser Ile Asn  
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Glu Asn Cys Gln Val Pro Glu Glu Asp Phe Pro Val Val Asn Tyr  
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Pro Val Asn

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